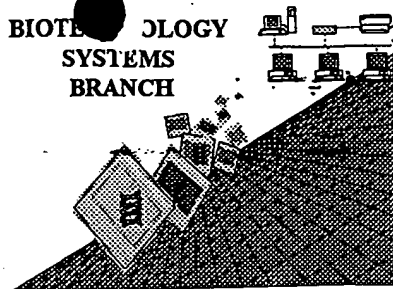


Noted



BIOTECHNOLOGY
SYSTEMS
BRANCH



#7

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/367,013A

Source: 1652

Date Processed by STIC: 7/31/2000

RECEIVED

FEB 22 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



SEQUENCE LISTING

PATENT APPLICATION: US/09/367,013A

DATE: 08/01/2000

TIME: 16:10:58

Input Set : A:\Cgabl.app

Output Set: N:\CRF3\08012000\I367013A.raw

1652
Does Not Comply
Corrected Diskette Needed

see
P.5, too

3 <110> APPLICANT: KNUTZON, DEBORAH
4 MUKERJI, PRADIP
5 HUANG, YUNG-SHENG
6 THURMOND, JENNIFER
7 CHAUDHARY, SUNITA
8 LEONARD, AMANDA E.
10 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS OF LONG CHAIN
11 POLYUNSATURATED FATTY ACIDS
13 <130> FILE REFERENCE: CGAB-210 USA
15 <140> CURRENT APPLICATION NUMBER: 09/367,013A
16 <141> CURRENT FILING DATE: 1999-08-05
18 <150> PRIOR APPLICATION NUMBER: 08/834,655
19 <151> PRIOR FILING DATE: 1997-04-11
21 <160> NUMBER OF SEQ ID NOS: 40
23 <170> SOFTWARE: PatentIn Ver. 2.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1617
27 <212> TYPE: DNA
28 <213> ORGANISM: Mortierella alpina
30 <220> FEATURE:
31 <223> OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
33 <400> SEQUENCE: 1
34 cgacactcct tcctttcttct cacc
35 acaacaaacc atggctgctg ctcc
36 tgccgaggct ctgaatgagg gcaa
37 caacaagggtg tacgatgtcc gcga
38 caagcacgtt ggcaaggacg gcac
39 ggagactctt gccaaactttt acgt
40 tgatgaacttt gcggccgagg tccg
41 cgattcttcc aaggcatact acgcc
42 gtcgacggtc attgtggcca agtgg
43 tgcgcttttg ggtctgttct ggcag
44 ccagggtcttc caggaccgtt tctgg
45 ccagggtctc tcttctctgt ggtgg
46 cgtccacggc gaggatcccg acatt
47 gttggagatg ttctcggatg tccca
48 ggtcctgaac cagacctggt ttatc
49 cctccagtcg attctctttg tgctg
50 tgtgcccacg tctgttggtc agcag
51 caccatgttc ctgttcacga aggat
52 ggcgggtgtg ggaaacttgt tggcg
53 gatctcgaag gaggaggcgg tcgat
54 tgatgtccac ccgggtctat ttgcc
55 gcaccacttg ttcccttcga tgcct
56 gaccctgtgc aaaaagtaca atgtcc
57 agaggctctt agccgtctga acgag
58 gtaaaaaaaaa aaacaaggac gttttt

↑
Nucleotide
Sequence
↓

← no response shown.

Response is mandatory
when sequence
is combined DNA/RNA.

see 1.823 of
new sequence
Rebar

TC1
08/01/2000
16:10:58

RAW SEQUENCE LISTING

DATE: 08/01/2000

PATENT APPLICATION: US/09/367,013A

TIME: 16:10:58

Input Set : A:\Cgabl.app

Output Set: N:\CRF3\08012000\I367013A.raw

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59 tgtcaagtcg agcggtttctg gaaaggatcg ttcagtgacg tatcatcatt ctccttttac 1560
60 cccccgtca tatctcattc attctctctt ttaaacact tgttcccccc ttcaccg 1617
63 <210> SEQ ID NO: 2
64 <211> LENGTH: 457
65 <212> TYPE: PRT
66 <213> ORGANISM: Mortierella alpina
68 <400> SEQUENCE: 2
69 Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu Val Leu
70 1 5 10 15
72 Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe
73 20 25 30
75 Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro
76 35 40 45
78 Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly
79 50 55 60
81 Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu
82 65 70 75 80
84 Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys
85 85 90 95
87 Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln
88 100 105 110
90 Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val
91 115 120 125
93 Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys
94 130 135 140
96 Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu
97 145 150 155 160
99 Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His
100 165 170 175
102 His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe
103 180 185 190
105 Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys
106 195 200 205
108 His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp
109 210 215 220
111 Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met
112 225 230 235 240
114 Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe
115 245 250 255
117 Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala
118 260 265 270
120 Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly
121 275 280 285
123 Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu
124 290 295 300
126 Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe
127 305 310 315 320
129 Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser
130 325 330 335

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RAW SEQUENCE LISTING DATE: 08/01/2000
 PATENT APPLICATION: US/09/367,013A TIME: 16:10:58

Input Set : A:\Cgabl.app
 Output Set: N:\CRF3\08012000\I367013\raw

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132 Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His
133           340           345           350
135 Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe
136           355           360           365
138 Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe
139           370           375           380
141 Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu
142 385           390           395           400
144 Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val
145           405           410           415
147 Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met
148           420           425           430
150 Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys
151           435           440           445
153 Ala Ala Ser Lys Met Gly Lys Ala Gln
154           450           455
157 <210> SEQ ID NO: 3
158 <211> LENGTH: 1488
159 <212> TYPE: DNA
160 <213> ORGANISM: Mortierella alpina
162 <400> SEQUENCE: 3
163 gtccctgtgc gctgtgggca caccocatcc tccctcgtc cctctgcgtt tgccttggc 60
164 ccaccgtctc tctccaccc tccgagacga ctgcaactgt aatcaggaac cgacaaatac 120
165 acgatttctt tttactcagc accaactcaa aatcctcaac cgcaaccctt tttcaggatg 180
166 gcaactccca acactatcga tgccggtttg acccagcgtc atatcagcac ctccggcccca 240
167 aactcggcca agcctgcctt cgagcgcaac taccagctcc ccgagttcac catcaaggag 300
168 atccgagagt gcateccctgc ccaactgctt gagcgctccg gtctccgttg tctctgccac 360
169 gttgccatcg atctgacttg ggcgtcgctc ttgttccctg ctgcgaccca gatcgacaag 420
170 tttgagaatc ccttgatccg ctatttggcc tggcctggtt actggatcat gcagggtatt 480
171 gtctgcaccg gtgtctgggt gctggctcac gagtgtggtc atcagtcctt ctcgacctcc 540
172 aagacctca acaacacagt tggttggatc ttgcaactga tgccttgggt cccctaccac 600
173 tccctggagaa tctcgactc gaagcaccac aaggccactg gccatatgac caaggaccag 660
174 gtctttgtgc ccaagaccg ctcccagggt ggcttgctc ccaaggagaa cgctgctgct 720
175 gccgttcagg aggaggacat gtccgtgcac ctggatgagg aggcctccat tgtgactttg 780
176 ttctggatgg tgatccagtt ctgttccgga tggcccgctg acctgattat gaacgcctct 840
177 ggccaagact acggccgctg gacctcgcac ttccacacgt actcgcccat ctttgagccc 900
178 cgcaactttt tcgacattat tatctcggac ctccgtgtgt tggctgccct cggtgccctg 960
179 atctatgcct ccattgcagtt gtcgtctctg accgtcacca agtactatat tgtcccttac 1020
180 ctctttgtca acttttggtt gtcctgata acctcttgc agcacaccga tcccaagctg 1080
181 cccattacc gcgaggtgtc ctggaatttc cagcgtggag ctctttgcac cgttgaccgc 1140
182 tcgtttggca agttcttggg ccatatgttc cagggcattg tccacacca tgtggcccat 1200
183 cacttggtct cgcaaatgcc gttctaccat gctgaggaag ctacctatca tctcaagaaa 1260
184 ctgctgggag agtactatgt gtacgaccca tcccgatcg tcgttgcggt ctggaggctg 1320
185 ttccgtgagt gccgattcgt ggaggatcag ggagacgtgg tctttttcaa gaagtaaaaa 1380
186 aaaagacaat ggaccacaca caacctgtgc tctacagacc tacgtatcat gtaccatac 1440
187 cacttcataa aagaacatga gctctagagg cgtgtcattc gcgcctcc 1488
190 <210> SEQ ID NO: 4
191 <211> LENGTH: 399
192 <212> TYPE: PRT

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RAW SEQUENCE LISTING

DATE: 08/01/2000

PATENT APPLICATION: US/09/367,013A

TIME: 16:10:58

Input Set : A:\Cgabl.app

Output Set: N:\CRF3\08012000\I367013A.raw

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193 <213> ORGANISM: Mortierella alpina
195 <400> SEQUENCE: 4
196 Met Ala Pro Pro Asn Thr Ile Asp Ala Gly Leu Thr Gln Arg His Ile
197   1           5           10           15
199 Ser Thr Ser Ala Pro Asn Ser Ala Lys Pro Ala Phe Glu Arg Asn Tyr
200           20           25           30
202 Gln Leu Pro Glu Phe Thr Ile Lys Glu Ile Arg Glu Cys Ile Pro Ala
203           35           40           45
205 His Cys Phe Glu Arg Ser Gly Leu Arg Gly Leu Cys His Val Ala Ile
206           50           55           60
208 Asp Leu Thr Trp Ala Ser Leu Leu Phe Leu Ala Ala Thr Gln Ile Asp
209   65           70           75           80
211 Lys Phe Glu Asn Pro Leu Ile Arg Tyr Leu Ala Trp Pro Val Tyr Trp
212           85           90           95
214 Ile Met Gln Gly Ile Val Cys Thr Gly Val Trp Val Leu Ala His Glu
215           100          105          110
217 Cys Gly His Gln Ser Phe Ser Thr Ser Lys Thr Leu Asn Asn Thr Val
218           115          120          125
220 Gly Trp Ile Leu His Ser Met Leu Leu Val Pro Tyr His Ser Trp Arg
221           130          135          140
223 Ile Ser His Ser Lys His His Lys Ala Thr Gly His Met Th Lys Asp
224  145          150          155          160
226 Gln Val Phe Val Pro Lys Thr Arg Ser Gln Val Gly Leu Pro Pro Lys
227           165          170          175
229 Glu Asn Ala Ala Ala Val Gln Glu Asp Met Ser Val His Leu
230           180          185          190
232 Asp Glu Glu Ala Pro Ile Val Thr Leu Phe Trp Met Val Ile Gln Phe
233           195          200          205
235 Leu Phe Gly Trp Pro Ala Tyr Leu Ile Met Asn Ala Ser Gly Gln Asp
236           210          215          220
238 Tyr Gly Arg Trp Thr Ser His Phe His Thr Tyr Ser Pro Ile Phe Glu
239  225          230          235          240
241 Pro Arg Asn Phe Phe Asp Ile Ile Ile Ser Asp Leu Gly Val Leu Ala
242           245          250          255
244 Ala Leu Gly Ala Leu Ile Tyr Ala Ser Met Gln Leu Ser Leu Leu Thr
245           260          265          270
247 Val Thr Lys Tyr Tyr Ile Val Pro Tyr Leu Phe Val Asn Phe Trp Leu
248           275          280          285
250 Val Leu Ile Thr Phe Leu Gln His Thr Asp Pro Lys Leu Pro His Tyr
251           290          295          300
253 Arg Glu Gly Ala Trp Asn Phe Gln Arg Gly Ala Leu Cys Thr Val Asp
254  305          310          315          320
256 Arg Ser Phe Gly Lys Phe Leu Asp His Met Phe His Gly Ile Val His
257           325          330          335
259 Thr His Val Ala His His Leu Phe Ser Gln Met Pro Phe Tyr His Ala
260           340          345          350
262 Glu Gln Ala Thr Tyr His Leu Lys Lys Leu Leu Gly Glu Tyr Tyr Val
263           355          360          365
265 Tyr Asp Pro Ser Pro Ile Val Val Ala Val Trp Arg Ser Phe Arg Glu

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/367,013A
 DATE: 08/01/2000
 TIME: 16:10:58

Input Set : A:\Cgabl.app
 Output Set: N:\CRF3\08012000\I367013A.raw

```

266      370      375      380
268 Cys Arg Phe Val Glu Asp Gln Gly Asp Val Val Phe Phe Lys Lys
269 385      390      395
272 <210> SEQ ID NO: 5
273 <211> LENGTH: 355
274 <212> TYPE: PRT
275 <213> ORGANISM: Mortierella alpina
277 <400> SEQUENCE: 5
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279 1      10      15
281 Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val Ser Phe Asn Leu Cys Ile
282      20      25      30
284 Trp Gly Leu Ser Thr Val Ile Val Ala Lys Trp Gly Gln Thr Ser Thr
285      35      40      45
287 Leu Ala Asn Val Leu Ser Ala Ala Leu Leu Gly Leu Phe Trp Gln Gln
288      50      55      60
290 Cys Gly Trp Leu Ala His Asp Phe Leu His His Gln Val Phe Gln Asp
291 65      70      75      80
293 Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe Leu Gly Gly Val Cys Gln
294      85      90      95
296 Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys His Asn Thr His His Ala
297      100      105      110
299 Ala Pro Asn Val His Gly Glu Asp Pro Asp Ile Asp Thr His Pro Leu
300      115      120      125
302 Leu Thr Trp Ser Glu His Ala Leu Glu Met Phe Ser Asp Val Pro Asp
303      130      135      140
305 Glu Glu Leu Thr Arg Met Trp Ser Arg Phe Met Val Leu Asn Gln Thr
306 145      150      155      160
308 Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala Arg Leu Ser Trp Cys Leu
309      165      170      175
311 Gln Ser Ile Leu Phe Val Leu Pro Asn Gly Gln Ala His Lys Pro Ser
312      180      185      190
314 Gly Ala Arg Val Pro Ile Ser Leu Val Glu Gln Leu Ser Leu Ala Met
315      195      200      205
317 His Trp Thr Trp Tyr Leu Ala Thr Met Phe Leu Phe Ile Lys Asp Pro
318      210      215      220
320 Val Asn Met Leu Val Tyr Phe Leu Val Ser Gln Ala Val Cys Gly Asn
321 225      230      235      240
323 Leu Leu Ala Ile Val Phe Ser Leu Asn His Asn Gly Met Pro Val Ile
324      245      250      255
326 Ser Lys Glu Glu Ala Val Asp Met Asp Phe Phe Thr Lys Gln Ile Ile
327      260      265      270
329 Thr Gly Arg Asp Val His Pro Gly Leu Phe Ala Asn Trp Phe Thr Gly
330      275      280      285
332 Gly Leu Asn Tyr Gln Ile Glu His His Leu Phe Pro Ser Met Pro Arg
333      290      295      300
335 His Asn Phe Ser Lys Ile Gln Pro Ala Val Glu Thr Leu Cys Lys Lys
336 305      310      315      320
338 Tyr Asn Val Arg Tyr His Thr Thr Gly Met Ile Glu Gly Thr Ala Glu

```

File I
↓

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 08/01/2000

PATENT APPLICATION: US/09/367,013A

TIME: 16:10:59

Input Set : A:\Cgabl.app

Output Set: N:\CRF3\08012000\I367013A.raw

L:360 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
 L:360 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
 L:360 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
 L:363 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
 L:363 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
 M:340 Repeated in SeqNo=6
 L:366 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
 L:366 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
 L:444 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
 L:444 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
 L:444 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
 L:447 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
 L:447 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
 M:340 Repeated in SeqNo=8
 L:465 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
 L:465 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
 L:493 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:9
 L:493 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
 L:493 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
 L:493 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
 L:493 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
 L:558 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
 L:558 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
 L:558 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
 L:726 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:20
 L:726 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20
 L:726 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20
 L:736 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:21
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 L:736 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
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 L:744 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
 L:757 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
 L:757 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22
 L:757 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
 L:760 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:22
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 M:340 Repeated in SeqNo=22
 L:1173 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/367,013A

DATE: 08/01/2000

TIME: 16:10:59

Input Set : A:\Cgabl.app

Output Set: N:\CRF3\08012000\I367013A.raw

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M:340 Repeated in SeqNo=34
L:1182 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:34
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L:1330 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:37
L:1401 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38
M:340 Repeated in SeqNo=3
L:1529 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:39
M:340 Repeated in SeqNo=39
L:1684 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40
M:340 Repeated in SeqNo=40



Application No.: 09/367,013

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

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